

1	CGGCACGAGGGCATGGGGCGGCTGGTTCTGCTGTGGGGAGCTGCCGTCTTTCTGCTGGGA	60
1	M G R L V L L W G A A V F L L G	16
61	GGCTGGATGGCTTTGGGGCAAGGAGGAGCAGCAGAAGGAGTACAGATTGATCATCTAC	120
17	G W M A L G Q G G A A E G V Q I Q I I Y	36
121	TTCAATTTAGAAACCGTGCAGGTGACATGGAATGCCAGCAAATACTCCAGGACCAACCTG	180
37	F N L E T V Q V T W N A S K Y S R T N L	56
181	ACTTTCCACTACAGATTCAACGGTGATGAGGCCTATGACCAGTGCACCAACTACCTTCTC	240
57	T F H Y R F N G D E A Y D Q C T N Y L L	76
241	CAGGAAGGTCACACTTCGGGGTGCCTCCTAGACGCAGAGCAGCGAGACGACATTCTCTAT	300
77	Q E G H T S G C L L D A E Q R D D I L Y	96
301	TTCTCCATCAGGAATGGGACGCACCCCGTTTTTCACCGCAAGTCGCTGGATGGTTTATTAC	360
97	F S I R N G T H P V F T A S R W M V Y Y	116
361	CTGAAACCCAGTTCCCCGAAGCACGTGAGATTTTCGTGGCATCAGGATGCAGTGACGGTG	420
117	L K P S S P K H V R F S W H Q D A V T V	136
421	ACGTGTTCTGACCTGTCTTACGGGGATCTCCTCTATGAGGTTTCAGTACCGGAGCCCTTC	480
137	T C S D L S Y G D L L Y E V Q Y R S P F	156
481	GACACCGAGTGGCAGTCCAAACAGGAAAATACCTGCAACGTCACCATAGAAGGCTTGGAT	540
157	D T E W Q S K Q E N T C N V T I E G L D	176
541	GCCGAGAAGTGTACTCTTTCTGGGTGAGGGTGAAGGCTATGGAGGATGTATATGGGCCA	600
177	A E K C Y S F W V R V K A M E D V Y G P	196
601	GACACATACCCAAGCGACTGGTCAGAGGTGACATGCTGGCAGAGAGCGGAGATTTCGGGAT	660
197	D T Y P S D W S E V T C W Q R G E I R D	216
661	GCCTGTGCAGAGACACCAACGCCTCCCAAACCAAGCTGTCCAAATTTATTTTAATTTC	720
217	A C A E T P T P P K P K L S K F I L I S	236
721	AGCCTGGCCATCCTTCTGATGGTGTCTCTCCTCTCTGTCTTTATGGAAATTATGGAGA	780
237	S L A I L L M V S L L L L S L W K L W R	256
781	GTGAAGAAGTTTCTCATTTCCAGCGTGCCAGACCCGAAATCCATCTTCCCGGGCTCTTT	840
257	V K K F L I P S V P D P K S I F P G L F	276
841	GAGATACACCAAGGGAACCTCCAGGAGTGGATCACAGACACCCAGAACGTGGCCACCTC	900
277	E I H Q G N F Q E W I T D T Q N V A H L	296

FIG. 1A

901 CACAAGATGGCAGGTGCAGAGCAAGAAAGTGGCCCCGAGGAGCCCCTGGTAGTCCAGTTG 960
 297 H K M A G A E Q E S G P E E P L V V Q L 316

 961 GCCAAGACTGAAGCCGAGTCTCCAGGATGCTGGACCCACAGACCGAGGAGAAAGAGGCC 1020
 317 A K T E A E S P R M L D P Q T E E K E A 336

 1021 TCTGGGGGATCCCTCCAGCTTCCCCACCAGCCCCCTCCAAGGCGGTGATGTGGTCACAATC 1080
 337 S G G S L Q L P H Q P L Q G G D V V T I 356

 1081 GGGGGCTTCACCTTTGTGATGAATGACCGCTCCTACGTGGCGTTGTGATGGACACACCAC 1140
 357 G G F T F V M N D R S Y V A L * 372

 1141 TGTCAAAGTCAACGTCAGGATCCACGTTGACATTTAAAGACAGAGGGGACTGTCCCGGGG 1200

 1201 ACTCCACACCACCATGGATGGGAAGTCTCCACGCCAATGATGGTAGGACTAGGAGACTCT 1260

 1261 GAAGACCCAGCCTCACCGCCTAATGCGGCCACTGCCCTGCTAACTTTCCCCCACATGAGT 1320

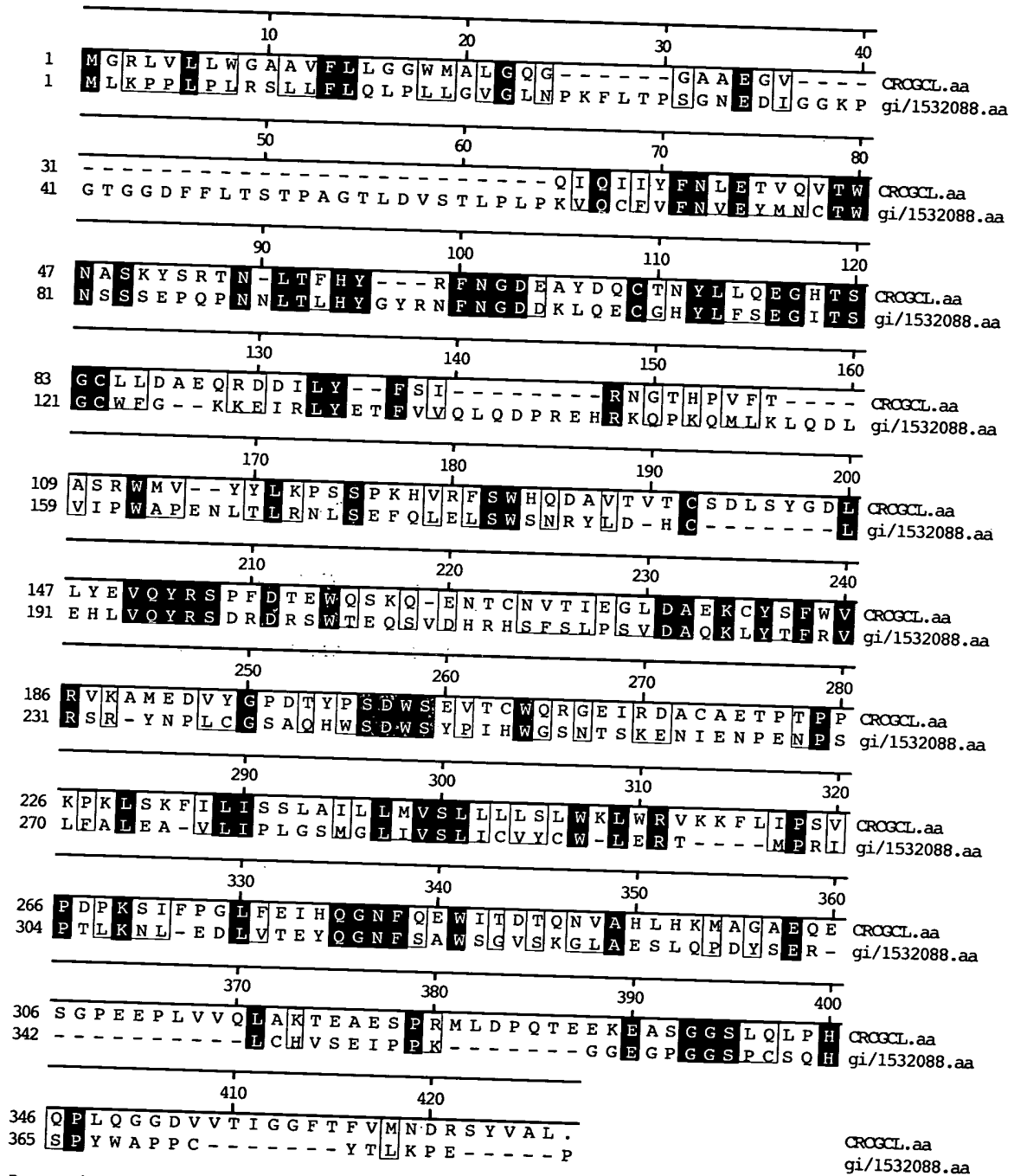
 1321 CTCTGTGTTCAAAGGCTTGATGGCAGATGGGAGCCAATTGCTCCAGGAGATTTACTCCCA 1380

 1381 GTTCCTTTTCGTGCCTGAACGTTGTCACATAAACCCCAAGGCAGCACGTCCAAAATGCTG 1440

 1441 TAAAACCATCTTCCCACTCTGTGAGTCCCCAGTTCCGTCCATGTACCTGTTCCATAGCAT 1500

 1501 TGGATTCTCGGAGGATTTTTGTCTGTTTGAGACTCCAAACCACCTCTACCCCTACAAA 1560

 1561 AAAAAAAAAAAAAA 1573



Decoration 'Decoration #1': Box residues that match the consensus named 'Consensus #2' exactly.

Decoration 'Decoration #2': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 2

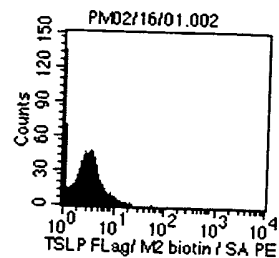
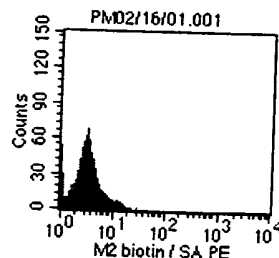
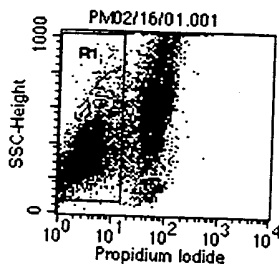
Transfection, Stat5b IP followed by PY Western

	pC4	IL7	IL7+Fc	TSLP(10x)	pc4	TSLP(10x)	TSLP +Fc	pC4	TSLP(10x)	TSLP +Fc	IL2	TSLP(10x)
Stat5b	-	+	-	-	-	+	-	-	+	-	+	-
IL7R α	-	+	-	-	-	+	-	-	+	-	+	-
IL2R β	-	-	-	-	-	-	-	-	-	-	-	-
Jak2	-	-	-	-	-	-	-	-	+	-	+	-
Jak3	-	+	-	-	-	-	-	-	+	-	-	-
Tyk2	-	-	-	-	-	+	-	-	-	-	-	-
IL2 γ_c	-	-	+	-	-	-	-	-	+	-	+	-
CRCGCL	-	-	-	-	+	+	-	-	+	-	+	-
pCDNA3	+	-	-	-	+	-	-	+	-	-	+	-

Arrows pointing to specific bands in the Western blot:

- Jak2
- Tyk2
- STAT5

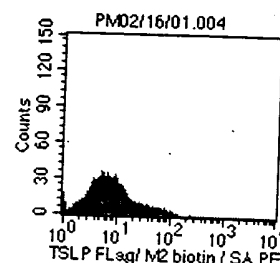
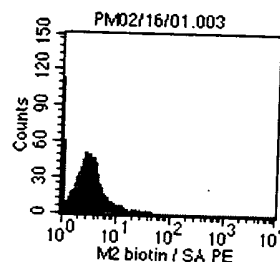
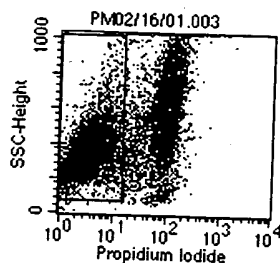
PC4



Mean
3.56

Mean
3.56

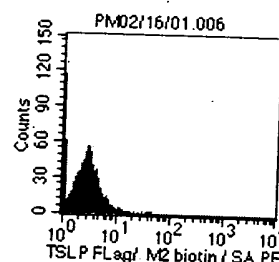
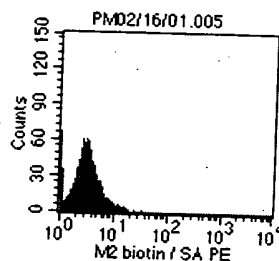
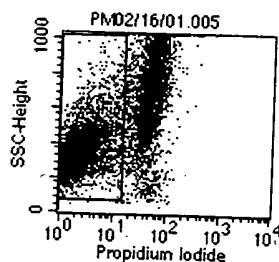
CRCGCL



Mean
3.69

Mean
11.20

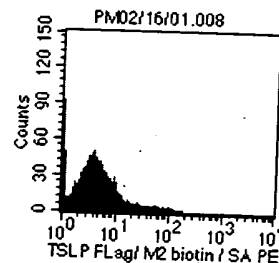
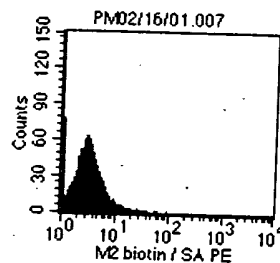
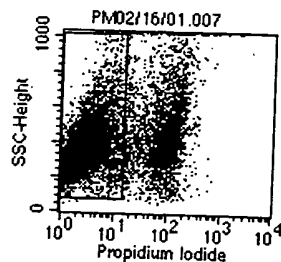
IL2 common
gamma C



Mean
3.50

Mean
3.22

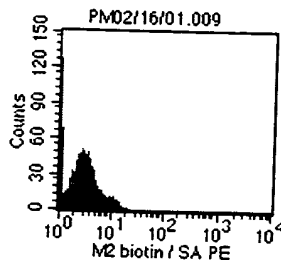
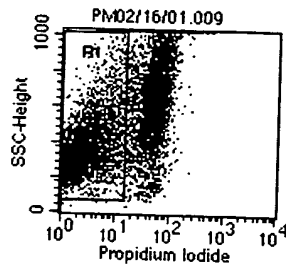
CRCGCL
+ IL7a



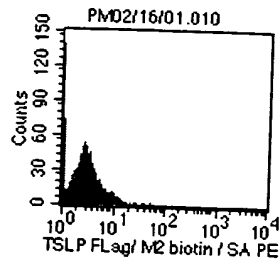
Mean
3.57

Mean
7.23

IL7a

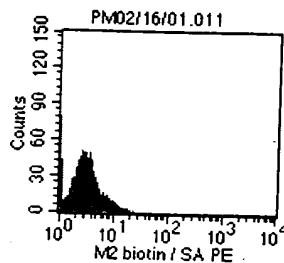
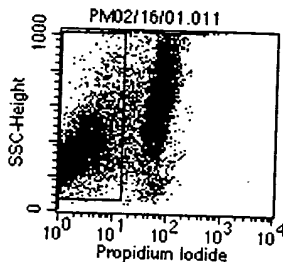


Mean
3.46

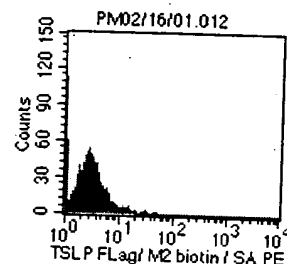


Mean
3.41

IL2 common
gamma C + IL7a



Mean
3.60



Mean
3.41